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RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/075,446

TIME: 10:12:39

Input Set : N:\Crf3\RULE60\10075446.raw

Output Set: N:\CRF3\04242002\J075446.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: RUBEN, STEVEN M.

6 JIMENEZ, PABLO

7 DUAN, D. ROXANNE

8 RAMPY, MARK A.

9 MENDRICK, DONNA

10 ZHANG, JUN

11 NI, JIAN

12 MOORE, PAUL A.

13 COLEMAN, TIMOTHY A.

14 GRUBER, JOACHIM R.

W--> 15 DILLON, PATRICK J.

W--> 16 GENTZ, REINER L.

18 (ii) TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

20 (iii) NUMBER OF SEQUENCES: 148

22 (iv) CORRESPONDENCE ADDRESS:

23 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

24 (B) STREET: 1100 NEW YORK AVE, NW, SUITE 600

25 (C) CITY: WASHINGTON

26 (D) STATE: DC

27 (E) COUNTRY: USA

28 (F) ZIP: 20005-3934

30 (v) COMPUTER READABLE FORM:

31 (A) MEDIUM TYPE: Floppy disk

32 (B) COMPUTER: IBM PC compatible

33 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

34 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

36 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/075,446

C--> 37 (B) FILING DATE: 15-Feb-2002

C--> 38 (C) CLASSIFICATION:

70 (vii) PRIOR APPLICATION DATA:

42 (A) APPLICATION NUMBER: 09/023,082

43 (B) FILING DATE:

47 (A) APPLICATION NUMBER: PCT/US95/01790

48 (B) FILING DATE: 14-FEB-1995

51 (A) APPLICATION NUMBER: US 08/461,195

52 (B) FILING DATE: 05-JUN-1995

55 (A) APPLICATION NUMBER: US 60/023,852

56 (B) FILING DATE: 13-AUG-1996

59 (A) APPLICATION NUMBER: US 60/039,045

60 (B) FILING DATE: 28-FEB-1997

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63      (A) APPLICATION NUMBER: US 08/862,432
64      (B) FILING DATE: 23-MAY-1997
67      (A) APPLICATION NUMBER: US 08/910,875
68      (B) FILING DATE: 13-AUG-1997
71      (A) APPLICATION NUMBER: US 60/055,561
72      (B) FILING DATE: 13-AUG-1997
74      (viii) ATTORNEY/AGENT INFORMATION:
75          (A) NAME: STEFFFE, ERIC K.
76          (B) REGISTRATION NUMBER: 36,688
77          (C) REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
79      (ix) TELECOMMUNICATION INFORMATION:
80          (A) TELEPHONE: 202-371-2600
81          (B) TELEFAX: 202-371-2540
83      (2) INFORMATION FOR SEQ ID NO: 1:
85          (i) SEQUENCE CHARACTERISTICS:
86              (A) LENGTH: 627 base pairs
87              (B) TYPE: nucleic acid
88              (C) STRANDEDNESS: double
89              (D) TOPOLOGY: both
91          (ii) MOLECULE TYPE: DNA (genomic)
94          (ix) FEATURE:
95              (A) NAME/KEY: CDS
96              (B) LOCATION: 1..624
99          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
101  ATG TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG      48
102  Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
103    1          5          10          15
105  CCC GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC      96
106  Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
107          20          25          30
109  GTC CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG      144
110  Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
111    35          40          45
113  GCC ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA      192
114  Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
115    50          55          60
117  AGG CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA      240
118  Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
119    65          70          75          80
121  AAG CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG      288
122  Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
123          85          90          95
125  AAG GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG      336
126  Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
127          100          105          110
129  ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC      384
130  Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
131    115          120          125
133  AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA      432

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134 Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
135      130      135      140
137 GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA      480
138 Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
139 145      150      155      160
141 TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG      528
142 Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
143      165      170      175
145 TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA      576
146 Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
147      180      185      190
149 CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA      624
150 Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
151      195      200      205
153 TAG      627
156 (2) INFORMATION FOR SEQ ID NO: 2:
158     (i) SEQUENCE CHARACTERISTICS:
159         (A) LENGTH: 208 amino acids
160         (B) TYPE: amino acid
161         (D) TOPOLOGY: linear
163     (ii) MOLECULE TYPE: protein
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
167 Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
168 1      5      10      15
170 Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
171      20      25      30
173 Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
174      35      40      45
176 Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
177      50      55      60
179 Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
180 65      70      75      80
182 Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
183      85      90      95
185 Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
186      100      105      110
188 Ile Thr Ser Val Glu Ile Gly Val Ala Val Lys Ala Ile Asn Ser
189      115      120      125
191 Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
192      130      135      140
194 Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
195 145      150      155      160
197 Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
198      165      170      175
200 Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
201      180      185      190
203 Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
204      195      200      205
207 (2) INFORMATION FOR SEQ ID NO: 3:

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/075,446

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Input Set : N:\Crif3\RULE60\10075446.raw

Output Set: N:\CRF3\04242002\J075446.raw

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209      (i) SEQUENCE CHARACTERISTICS:
210          (A) LENGTH: 36 base pairs
211          (B) TYPE: nucleic acid
212          (C) STRANDEDNESS: single
213          (D) TOPOLOGY: linear
215      (ii) MOLECULE TYPE: cDNA
220      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
222 CCCACATGT GGAAATGGAT ACTGACACAT TGTGCC      36
224 (2) INFORMATION FOR SEQ ID NO: 4:
226      (i) SEQUENCE CHARACTERISTICS:
227          (A) LENGTH: 35 base pairs
228          (B) TYPE: nucleic acid
229          (C) STRANDEDNESS: single
230          (D) TOPOLOGY: linear
232      (ii) MOLECULE TYPE: cDNA
237      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
239 CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG      35
241 (2) INFORMATION FOR SEQ ID NO: 5:
243      (i) SEQUENCE CHARACTERISTICS:
244          (A) LENGTH: 36 base pairs
245          (B) TYPE: nucleic acid
246          (C) STRANDEDNESS: single
247          (D) TOPOLOGY: linear
249      (ii) MOLECULE TYPE: cDNA
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
256 CATGCCATGG CGTGCCAAGC CCTTGGTCAG GACATG      36
258 (2) INFORMATION FOR SEQ ID NO: 6:
260      (i) SEQUENCE CHARACTERISTICS:
261          (A) LENGTH: 35 base pairs
262          (B) TYPE: nucleic acid
263          (C) STRANDEDNESS: single
264          (D) TOPOLOGY: linear
266      (ii) MOLECULE TYPE: cDNA
271      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
273 CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG      35
275 (2) INFORMATION FOR SEQ ID NO: 7:
277      (i) SEQUENCE CHARACTERISTICS:
278          (A) LENGTH: 35 base pairs
279          (B) TYPE: nucleic acid
280          (C) STRANDEDNESS: single
281          (D) TOPOLOGY: linear
283      (ii) MOLECULE TYPE: cDNA
288      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
290 GCGGGATCCG CCATCATGTG GAAATGGATA CTCAC      35
292 (2) INFORMATION FOR SEQ ID NO: 8:
294      (i) SEQUENCE CHARACTERISTICS:
295          (A) LENGTH: 27 base pairs
296          (B) TYPE: nucleic acid
297          (C) STRANDEDNESS: single

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PATENT APPLICATION: US/10/075,446

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Input Set : N:\Crf3\RULE60\10075446.raw

Output Set: N:\CRF3\04242002\J075446.raw

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298         (D) TOPOLOGY: linear
300     (ii) MOLECULE TYPE: cDNA
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
307 GCGCGGTACC ACAAACGTTG CCTTCCT
309 (2) INFORMATION FOR SEQ ID NO: 9:
311     (i) SEQUENCE CHARACTERISTICS:
312         (A) LENGTH: 40 base pairs
313         (B) TYPE: nucleic acid
314         (C) STRANDEDNESS: single
315         (D) TOPOLOGY: linear
317     (ii) MOLECULE TYPE: cDNA
322     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
324 TAACGAGGAT CCGCCATCAT GTGGAAATGG ATACTGACAC
326 (2) INFORMATION FOR SEQ ID NO: 10:
328     (i) SEQUENCE CHARACTERISTICS:
329         (A) LENGTH: 38 base pairs
330         (B) TYPE: nucleic acid
331         (C) STRANDEDNESS: single
332         (D) TOPOLOGY: linear
334     (ii) MOLECULE TYPE: cDNA
339     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
341 TAAGCACTCG AGTGAGTGTA CCACCATTGG AAGAAATG
343 (2) INFORMATION FOR SEQ ID NO: 11:
345     (i) SEQUENCE CHARACTERISTICS:
346         (A) LENGTH: 54 base pairs
347         (B) TYPE: nucleic acid
348         (C) STRANDEDNESS: single
349         (D) TOPOLOGY: linear
351     (ii) MOLECULE TYPE: cDNA
356     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
358 ATTAACCCTC ACTAAAGGGA GGCCATGTGG AAATGGATAC TGACACATTG TGCC
360 (2) INFORMATION FOR SEQ ID NO: 12:
362     (i) SEQUENCE CHARACTERISTICS:
363         (A) LENGTH: 35 base pairs
364         (B) TYPE: nucleic acid
365         (C) STRANDEDNESS: single
366         (D) TOPOLOGY: linear
368     (ii) MOLECULE TYPE: cDNA
373     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
375 CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG
377 (2) INFORMATION FOR SEQ ID NO: 13:
379     (i) SEQUENCE CHARACTERISTICS:
380         (A) LENGTH: 206 amino acids
381         (B) TYPE: amino acid
382         (C) STRANDEDNESS: Not Relevant
W--> 383         (D) TOPOLOGY: Not Relevant
385     (ii) MOLECULE TYPE: protein
390     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
392 Met Ser Gly Pro Gly Thr Ala Ala Val Ala Leu Leu Pro Ala Val Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/075,446

DATE: 04/24/2002

TIME: 10:12:40

Input Set : N:\Crf3\RULE60\10075446.raw

Output Set: N:\CRF3\04242002\J075446.raw

L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:15 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:16 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:437 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:491 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:557 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:602 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:647 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:702 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:756 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:811 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:871 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:1183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:1225 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:1246 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:2619 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
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L:2639 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
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L:3250 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=96
L:3573 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=112
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L:3797 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=120
L:3906 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=124
L:4015 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=128
L:4124 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=132
L:4233 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=136
L:4342 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=140
L:4483 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=146